Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	1252	"multiplex PCR"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/03/02 15:59
L2	134	L1 and "cell free"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/03/02 16:00
L3	28371	promoter and tag	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/03/02 16:00
L4	99	l2 and l3	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/03/02 16:00
L5	5056	"protein synthesis" and "cell free"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/03/02 16:00
L6	64	l4 and l5	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/03/02 16:00
L7	0	l6 and "second pcr"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/03/02 16:01
L8	2	"l64" and "second primer"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/03/02 16:12
L9	1339453	overlapping sequence	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/03/02 16:12
L10	4377	"overlapping sequence"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/03/02 16:13
L11	61	l10 and l1	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/03/02 16:13
L12	19	l11 and "second PCR"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/03/02 16:25

L13	11	"5655563".pn. or "552302".pn. or "5492817".pn. or "5324637".pn. or "4966964".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/03/02 16:26

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	2016	template SAME (universal or mega)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/02/25 14:26
L2	4359	"5' primer" SAME "3' primer"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/02/25 14:26
L3	15380	promoter SAME terminator	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/02/25 14:27
L4	10	l1 and l2 and l3	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/02/25 14:49
L5	10	l4 and "PCR"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/02/25 14:29
L6	0	"first sense primer" and "second sense primer"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/02/25 14:50
L7	10	"first 5' primer" and "second 5' primer"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/02/25 14:50
S1	3850	motoda.in. or yabuki.in. or kigawa.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2004/08/19 15:25
S2	20131	"template DNA" or (template NEAR2 DNA)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2004/08/19 15:26
S3	77799	"polymerase chain reaction" or PCR	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2004/08/19 15:26
S4	15885	(first or second or third) NEAR2 DNA	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2004/08/19 15:27

	U	Document ID	Title
1	X	US 20050032104 A1	Genome walking by selective amplification of nick-translate DNA library and amplification from complex mixtures of templates
2	X	US 20040214174 A1	Reactions on a solid surface
3	X	US 20040137484 A1	Nucleic acid amplification methods
4	X	US 20030190604 A1	Nucleic acid amplification method: ramification-extension amplification method (RAM)
5	X	US 20030175706 A1	Nucleic acid amplification methods
6	X	US 20030064376 A1	Genome walking by selective amplification of nick-translate DNA library and amplification from complex mixtures of templates
7	X	US 20030044796 A1	Reactions on dendrimers
8	X	US 20030040620 A1	Method of producing a DNA library using positional amplification
9	X	US 20020182598 A1	Nucleic acid amplification methods
10	X	US 6855523 B2	Nucleic acid amplification method: ramification-extension amplification method (RAM)
11	X	US 6828098 B2	Method of producing a DNA library using positional amplification based on the use of adaptors and nick translation

	U	Document ID	Title
12	X	US 6777187 B2	Genome walking by selective amplification of nick-translate DNA library and amplification from complex mixtures of templates
13	X	US RE38442 E	Nucleic acid amplification method hybridization signal amplification method (HSAM)
14	X	US 6692917 B2	Systems and methods for invasive cleavage reaction on dendrimers
15	X	US 6593086 B2	Nucleic acid amplification methods
16	X	US 6569647 B1	Nucleic acid amplification method: ramification-extension amplification method (RAM)
17	X	US 6110709 A	Cleaved amplified modified polymorphic sequence detection methods
18	X	US 5942391 A	Nucleic acid amplification method: ramification-extension amplification method (RAM)
19	X	US 5876924 A	Nucleic acid amplification method hybridization signal amplification method (HSAM)

	Document ID	Title
1	US 20040214174 A1	Reactions on a solid surface
2	US 20040126789 A1	Compositions and methods for synthesizing nucleic acids
3	US 20030228616 A1	DNA polymerase mutants with reverse transcriptase activity
4	US 20030175749 A1	Annealing control primer and its uses
5	US 20030104459 A1	Multiplex PCR
6	US 20030054338 A1	Detection of target sequences by cleavage of non-target nucleic acids
7	US 20030044796 A1	Reactions on dendrimers
8	US 6692917 B2	Systems and methods for invasive cleavage reaction on dendrimers
9	US 6673616 B1	Methods and compositions for characterizing nucleic acids
10	US 6372424 B1	Rapid detection and identification of pathogens
11	US 5843669 A	Cleavage of nucleic acid acid using thermostable methoanococcus jannaschii FEN-1 endonucleases

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on STN DUPLICATE 1

ACCESSION NUMBER: 2000412346 EMBASE
TITLE: Single-step single-molecule PCR of DNA with a homo-priming sequence using a single primer and hot-startable DNA polymerase.
AUTHOR: Nakano H.; Kobayashi K.; Ohuchi S.; Sekiguchi S.; Yamane T.
CORPORATE SOURCE: H. Nakano, Lab. of Molecular Biotechnology, Grad. Sch. of Biol. and Agric. Sci., Nagoya University, Furo-cho, Chikusa-ku, Nagoya 464-8601, Japan
SOURCE: Journal of Bioscience and Bioengineering, (2000) 90/4 (456-458).
Refs: 13
ISSN: 1389-1723 CODEN: JBBIF6
COUNTRY: Japan
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

AB We have previously reported that a **protein** library can be constructed by directly combining PCR amplification of a single DNA molecule and **cell-free protein synthesis**. To specifically amplify single DNA molecules, however, **two-step PCR** with nested primers was used.
Here we describe a simpler method for single-step amplification of a stogie molecule. The method involves the use of both hot-startable DNA polymerase and a DNA template that has homo-priming sequences at both ends for amplification using a single primer. These two modifications greatly decreased the possibility of formation and subsequent accumulation, respectively, of primer-dimers that inhibit the amplification of target template. In addition, a high-fidelity DNA polymerase was successfully used, resulting in the significant reduction of the accumulation of mutations during amplification.

=>

L49 ANSWER 3 OF 3 MEDLINE on STN
ACCESSION NUMBER: 92140411 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1779981
TITLE: A nested PCR followed by magnetic separation of amplified fragments for detection of Escherichia coli Shiga-like toxin genes.
AUTHOR: Olsvik O; Rimstad E; Hornes E; Strockbine N; Wasteson Y; Lund A; Wachsmuth K
CORPORATE SOURCE: Department of Microbiology and Immunology, Norwegian College of Veterinary Medicine, Oslo.
SOURCE: Molecular and cellular probes, (1991 Dec) 5 (6) 429-35. Journal code: 8709751. ISSN: 0890-8508.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199203
ENTRY DATE: Entered STN: 19920329
Last Updated on STN: 19920329
Entered Medline: 19920310

AB The Shiga-like toxin (SLT) I and II genes in cytotoxic Escherichia coli strains were detected using a polymerase chain reaction (PCR) procedure. Identification and differentiation of SLT I and II was carried out using primers giving PCR-generated DNA fragments of different size for the two cytotoxins. A **two-step PCR** procedure utilizing three primers in a nested configuration for both SLT I and II was combined with magnetic separation to identify the toxin genes in a rapid, specific and sensitive test system designated DIANA (Detection of Immobilized Amplified Nucleic Acid). The first PCR was carried out using standard methods, and the product generated was used as **primer** in the **second** PCR. In this procedure one of the primers from the first PCR was used with biotin label, and the **second** (inner) **primer** was 32P-labelled. The double-stranded DNA fragments generated containing the two primers, were biotinylated on one 5' end and 32P-labelled on the other 5' end. These fragments were separated from the solution using streptavidin-coated super-paramagnetic microscopic beads. The test could detect and differentiate between SLT I and II in a positive/negative ratio of more than 20. The assay could detect five SLT-positive E. coli organisms in the 5 microliters test sample. The presence of 100-fold more SLT-negative strains in a sample did not adversely affect the test signal.